



2121

## RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/032,260  
Source: OIPE  
Date Processed by STIC: 2/26/2002

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: [patin21help@uspto.gov](mailto:patin21help@uspto.gov) or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: [patin3help@uspto.gov](mailto:patin3help@uspto.gov) or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.1 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/ebc/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: U.S. Patent and Trademark Office, Box Sequence, P.O. Box 2327, Arlington, VA 22202
3. Hand Carry directly to:  
U.S. Patent and Trademark Office, Technology Center 1600, Reception Area, 7<sup>th</sup> Floor, Examiner Name, Sequence Information, Crystal Mall One, 1911 South Clark Street, Arlington, VA 22202  
Or  
U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202
4. Federal Express, United Parcel Service, or other delivery service to: U.S. Patent and Trademark Office, Box Sequence, Room 1B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

# Raw Sequence Listing Error Summary

## ERROR DETECTED

## SUGGESTED CORRECTION

SERIAL NUMBER: 10/032,260

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 ☐ Wrapped Nucleics  
Wrapped Aminos  
The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2 ☐ Invalid Line Length  
The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3 ☒ Misaligned Amino  
Numbering  
The numbering under each 5<sup>th</sup> amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
- 4 ☐ Non-ASCII  
The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5 ☐ Variable Length  
Sequence(s) contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6 ☐ PatentIn 2.0  
"bug"  
A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s). Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 7 ☐ Skipped Sequences  
(OLD RULES)  
Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence:  
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
(i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
This sequence is intentionally skipped  
Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
- 8 ☐ Skipped Sequences  
(NEW RULES)  
Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence.  
<210> sequence id number  
<400> sequence id number  
000
- 9 ☒ Use of n's or Xaa's  
(NEW RULES)  
Use of n's and/or Xaa's have been detected in the Sequence Listing.  
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.  
In <220> to <223> section, please explain location of n or Xaa; and which residue n or Xaa represents.
- 10 ☐ Invalid <213>  
Response  
Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
- 11 ☐ Use of <220>  
Sequence(s) missing the <220> "Feature" and associated numeric identifiers and responses.  
Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.  
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12 ☐ PatentIn 2.0  
"bug"  
Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
- 13 ☐ Misuse of n  
n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.



OIPE

## RAW SEQUENCE LISTING

DATE: 02/26/2002

PATENT APPLICATION: US/10/032,260

TIME: 11:05:42

Input Set : A:\EP.txt

Output Set: N:\CRF3\02262002\J032260.raw

pp 1-7

Does Not Comply  
Corrected Diskette Needed

3 <110> APPLICANT: de Belle, Ian  
4 Adamson, Eileen  
5 Mercola, Dan  
7 <120> TITLE OF INVENTION: Isolation and Identification of Control Sequences and  
8 Genes Modulated by Transcription Factors  
10 <130> FILE REFERENCE: PS-00101.P.1  
12 <140> CURRENT APPLICATION NUMBER: US/10/032,260  
13 <141> CURRENT FILING DATE: 2001-12-20  
15 <160> NUMBER OF SEQ ID NOS: 27  
17 <170> SOFTWARE: PatentIn Ver. 2.0

## ERRORED SEQUENCES

35 <210> SEQ ID NO: 3  
36 <211> LENGTH: 20  
37 <212> TYPE: PRT  
38 <213> ORGANISM: Homo sapiens  
40 <400> SEQUENCE: 3  
41 Cys Asp Asn Phe Ser Ala Tyr Gly Trp Cys Pro Leu Gly Pro Gln Cys  
E--> 42 1 5 5 10 10 15 15  
44 Pro Gln Ser His  
45 20  
47 <210> SEQ ID NO: 4  
48 <211> LENGTH: 31  
49 <212> TYPE: PRT  
50 <213> ORGANISM: Homo sapiens  
52 <400> SEQUENCE: 4  
53 Ile Ile Asp Thr Asp Glu Ala Ala Ala Glu Asp Lys Arg Arg Arg Arg  
E--> 54 1 5 10 15  
56 Arg Arg Arg Glu Lys Arg Lys Arg Ala Leu Leu Asn Leu Pro Gly  
E--> 57 20 25 30  
59 <210> SEQ ID NO: 5  
60 <211> LENGTH: 13  
61 <212> TYPE: PRT  
62 <213> ORGANISM: Homo sapiens  
64 <400> SEQUENCE: 5  
65 His Arg Ala Gly Phe Asp Ala Phe Met Thr Gly Tyr Val  
E--> 66 1 5 10  
221 <210> SEQ ID NO: 16  
222 <211> LENGTH: 234  
223 <212> TYPE: PRT  
224 <213> ORGANISM: Homo sapiens

misaligned amino  
acid numbers -  
see item 3 on  
Error Summary  
sheet - global  
error

same error

same

p. 2

## RAW SEQUENCE LISTING

DATE: 02/26/2002

PATENT APPLICATION: US/10/032,260

TIME: 11:05:42

Input Set : A:\EP.txt

Output Set: N:\CRF3\02262002\J032260.raw

226 <400> SEQUENCE: 16  
 227 Met Arg Asp His Ile Asp Tyr Arg Cys Cys Leu Pro Pro Ala Thr His  
 E--> 228 1 5 10 15  
 229 Arg Pro His Pro Thr Ser Ile Cys Asp Asn Phe Ser Ala Tyr Gly Trp  
 E--> 230 20 25 30 *same*  
 231 Cys Pro Leu Gly Pro Gln Cys Pro Gln Ser His Asp Ile Asp Pro Ile  
 E--> 232 35 40 45  
 233 Ile Asp Thr Asp Glu Ala Ala Ala Glu Asp Lys Arg Arg Arg Arg Arg  
 E--> 234 50 55 60  
 235 Arg Arg Glu Lys Arg Lys Arg Ala Leu Leu Asn Leu Pro Gly Thr Gln  
 E--> 236 65 70 75 80  
 237 Thr Ser Gly Glu Ala Lys Asp Gly Pro Pro Lys Lys Gln Val Cys Gly  
 E--> 238 85 90 95  
 239 Asp Ser Ile Lys Pro Glu Glu Thr Glu Gln Glu Val Ala Ala Asp Glu  
 E--> 240 100 105 110  
 241 Thr Arg Asn Leu Pro His Ser Lys Gln Gly Asn Lys Asn Asp Leu Glu  
 E--> 242 115 120 125  
 243 Met Gly Ile Lys Ala Ala Arg Pro Glu Ile Ala Asp Arg Ala Thr Ser  
 E--> 244 130 135 140  
 245 Glu Val Pro Gly Ser Gln Ala Ser Pro Asn Pro Val Pro Gly Gly Gly  
 E--> 246 145 150 155 160  
 247 Leu His Arg Ala Gly Phe Asp Ala Phe Met Thr Gly Tyr Val Met Ala  
 E--> 248 165 170 175  
 249 Tyr Val Glu Val Ser Gln Gly Pro Gln Pro Cys Ser Ser Gly Pro Trp  
 E--> 250 180 185 190  
 251 Leu Pro Glu Cys His Asn Lys Val Tyr Leu Ser Gly Lys Ala Val Pro  
 E--> 252 195 200 205  
 253 Leu Thr Val Ala Lys Ser Gln Phe Ser Arg Ser Ser Lys Ala His Asn  
 E--> 254 210 215 220  
 255 Gln Lys Met Lys Leu Thr Trp Gly Ser Ser  
 E--> 256 225 230  
 258 <210> SEQ ID NO: 17  
 259 <211> LENGTH: 725 *724 shown*  
 260 <212> TYPE: DNA  
 261 <213> ORGANISM: Homo sapiens  
 263 <400> SEQUENCE: 17  
 E--> 264 gnnngggggnr gnnnnngggg gaacttttat cggtgcctac tcacngaaaa ggctgaagag 60  
 265 tctcccatgt ctacttcttt ctacacagac acagcaacca tccgatttct caatcttttc 120  
 266 cccacctttc ccccttttct attccacaaa accgccattg tcatcatggg ccgtttctcaa 180  
 267 tgagctgttg ggtgagatat tagaattcta ctacagaaac gaaatgaaaa gtctcccatg 240  
 268 tctacttctt ctacacaaga cacagcaaca tccgatttct caatcttttc cccaactttc 300  
 E--> 269 ccccttttct antccacaan accgccattg tcatcatggg ncgtttctcaa tgagctgttg 360  
 270 ggtgagatat tagaattctg ggctgggaat gagttcagcc tgggtggaatg tgaacctgca 420  
 E--> 271 ncagtttggc atgaacgggc aaatgctgtg tancctccgg aaaggagcgc ttcctggaag 480  
 E--> 272 ctggcgcttg actttgtggg ngacatcctc cgggaaaang gttcactant tctaaagcgg 540  
 E--> 273 gcggaacgc ggtggggctc caattgcgcc taaantgngt ccgtattaca attcacnggg 600  
 E--> 274 cggccgtttt anaagtcttg nncggggaaa accnggggt anccaacttt atnccectgg 660  
 E--> 275 nngaaanccc ccttncnca acnggggtna naaccnannn gggcncnccn ntttgccect 720  
 E--> 276 cccaa 725 *724*

*see item 9 on Enol  
 Summary  
 sheet*

*item 9*

*item 9*

*659*

*719 nos. off*

## RAW SEQUENCE LISTING

DATE: 02/26/2002

PATENT APPLICATION: US/10/032,260

TIME: 11:05:42

Input Set : A:\EP.txt

Output Set: N:\CRF3\02262002\J032260.raw

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278 <210> SEQ ID NO: 18
279 <211> LENGTH: (619) 618 shown
280 <212> TYPE: DNA
281 <213> ORGANISM: Homo sapiens
283 <400> SEQUENCE: 18
284 agaagcttga attcgagcag agaagcttga attcgagcag aattggccca attttgcctt 60
285 ataccacttt ccaatacctt cacttggagt gacttacact gtggttaatt gcagttacaa 120
286 tgaagagatt aacatgggaa tgtcataata attgaatcta aagaagacat aatttcaaaa 180
287 taagagcttg agtaataata ccattgtgta acaatctgat ttccatccct cttatttttc 240
288 ctatattatg cagtttagtt ctttactatc atgtgtttca tgtttgttcg gttttaccaa 300
289 cacatcatta gtaaatgaa tgtaaggctt ctcatctctt ttgtatccta catctaaaag 360
290 attttagtcc ttagaatcct cttgaaatgt tctccattta aaatggagaa atagttcatg 420
E--> 291 ctctctcctc taagtangag ctaaaatcta aaaaattaat aaataaaata gtccatcctc 480
E--> 292 taataataat aatgaatact gaanttgtta antaataatt aatttttgag aaggggggtc 540
E--> 293 actaatgctg tccaagctgg agtgcaatgg cgtgatcact aanttctaaa ncggcgccaa 600
E--> 294 cgcggtggag ctccaantn (619) 618 (549) 549 numbering off
296 <210> SEQ ID NO: 19
297 <211> LENGTH: 716
298 <212> TYPE: DNA
299 <213> ORGANISM: Homo sapiens
301 <400> SEQUENCE: 19
E--> 302 ggngtgggng nnnngggggg ggnnttttng gnncggnnt tctnaagtnt cengggcctc 60
E--> 303 atnaaacagc gggccgagaa cgggnaana tgacaatggn ggttttgggg aatagaaaag 120
304 ggggaaaggt ggggaaatga ttgagaaatc ggatggttgc tgtgtctgtg tagaagaag 180
305 tagacatggg agacttttca ttttgttctg tgagtagaat tctgggctgg gaatgagttc 240
E--> 306 agcctggtga atgtgaacct gcaccagttt ggcataaacg gncagatgct gtgtaacctc 300
E--> 307 ggcaaggagc gcttctctga gctggcgctt gactttgtgg ggcacatcct ctggmacagg 360
E--> 308 ntccactagt tctagagcgg gcgccaccgc ggtggngctc caattegccc tanagtnggt 420
E--> 309 cgtnttaciaa ttcactggcc gtcgttttac aacgctctga ctgggaaaac cctggngtta 480
E--> 310 cccaacttaa tcgccttgca gcanatcccc ctttcgncag ctggngtnnt ancgangagg 540
E--> 311 nccgcaccgn ttgcccntcc caanaagttg cgcagcctgn atggggantg ggancgncct 600
E--> 312 gtnncgggng cantaaagcg gnggggtgtg gtgngtange ncancgtggn cgnnnnannt 660
E--> 313 gnnagnccct tangcngnn ccttcgnttc tcccttcctt cngnnnangt ngcggg 716
315 <210> SEQ ID NO: 20
316 <211> LENGTH: 619
317 <212> TYPE: DNA
318 <213> ORGANISM: Homo sapiens
320 <400> SEQUENCE: 20
321 agaagcttga attcgagcag agaagcttga attcgagcag aattggccca attttgcctt 60
322 ataccacttt ccaatacctt cacttggagt gacttacact gtggttaatt gcagttacaa 120
323 tgaagagatt aacatgggaa tgtcataata attgaatcta aagaagacat aatttcaaaa 180
324 taagagcttg agtaataata ccattgtgta acaatctgat ttccatccct cttatttttc 240
325 ctatattatg cagtttaagt tctttactat catgtgtttc atgtttgttc ggttttacc 300
E--> 326 acacatcatt agtaaatgga atgtangcct tctcatttct tttgtatcct acatctaaaa 360
327 gatttttagt tttagaatcc tcttgaaatg ttctccattt aaaatggaga aatagttcat 420
E--> 328 gctctctcat ctaantanga gctaaaatct aaaaaataaa taaataaaat antccatcct 480
E--> 329 ctaataataa taatgaatac tgaanttgtg aataataatt aatttttgag aatgggggtc 540
E--> 330 actaatgtcg tccaanctgg agtgcaatgg cgtgatcact agttctaaac cggcgccaac 600
E--> 331 gcggtgggnc tccaattcc 619

```

## RAW SEQUENCE LISTING

DATE: 02/26/2002

PATENT APPLICATION: US/10/032,260

TIME: 11:05:42

Input Set : A:\EP.txt

Output Set: N:\CRF3\02262002\J032260.raw

```

356 <210> SEQ ID NO: 22
357 <211> LENGTH: 419
358 <212> TYPE: DNA
359 <213> ORGANISM: Homo sapiens
361 <400> SEQUENCE: 22
362 acttgagtcaggagttcaa ggtgtagt agttgtgatt gcaacaacgc actccagcct 60
E--> 363 cgatgacaga gtgagaccct gtctgttaaa aaataataat aataatagat aatgggatan 120
E--> 364 gagtgtaaag aaagacagga tgccttcttag caaagttaca aaaaatatta atangtcttt 180
365 gtcacaataa tatgttttgc tatgagctga gaaagaaaaa tgaaaaagtg aaaataagat 240
E--> 366 ttctcaaggt acaactttga tgcagttcan gtcaaacctta ngtaagattt tgtttgtanag 300
367 tttgggaaat aaccattgtg gcaaggctgg aatgcaaatc gattttttgc tgttacagaa 360
368 acagttaaag aatttatggg attttatttt aatttagtta gctttttatg aggagaatt 419
387 <210> SEQ ID NO: 24
388 <211> LENGTH: 584
389 <212> TYPE: DNA
390 <213> ORGANISM: Homo sapiens
392 <400> SEQUENCE: 24
393 agagcagtc agtatatata catacatata caagctacaa gctgcatatg taattttaaaa 60
394 ttttctaata accacattta aaaaggtaaa aagaaactgt tgaaataaat tttaatatct 120
395 ttcatgaac ccaatatatg caaaatacta tcatttcaat tataaccaa ttaaaattaa 180
396 ggagatattt tacaattttc atattaacgt ttccaattct ggtgtgaatt ttacactcac 240
397 cgaacatctc aattctgaca agtcatttt taagtgctca acagctacgt gaggatagtg 300
E--> 398 gctattatgt cacaaaatgc agctctangg atgaggacag ttacagaag atacttgagg 360
E--> 399 atacaggagc aagttaaatg gcagtttaag aaagcaaatc cangatgtgg gaaactccac 420
E--> 400 agaatanatg acctggtttc tcccttact catcctcca aaatagaaat caatggcaga 480
E--> 401 aagaaaaaag anggaggctg ttgtancata aaatacttag ggacatacaa taaaacagt 540
E--> 402 gtagggtttt gttgaanccg attcactaca atgattcaca antt 584
404 <210> SEQ ID NO: 25
405 <211> LENGTH: 678
406 <212> TYPE: DNA
407 <213> ORGANISM: Homo sapiens
409 <400> SEQUENCE: 25
E--> 410 ggggnnnnn tnnngnaaat ctctngttc gggcccccc ancaaggtcg aggcctatcg 60
E--> 411 ataagctana tatcggaattc ctgcagccc ggggatctga tggttttata aaggggagtt 120
E--> 412 gccctgcgaa agctctctct tacctgcgc catgtaagac cggactttgc tcctcattag 180
E--> 413 gtcaccctag ccatgtggaa ctgtgagtc attaaacctc tttcctttat aaattatgca 240
E--> 414 gtctcgata tgtctttatt agcaagggtg aaatgaacta atacaagggt cacgtggtaa 300
E--> 415 atatatttaa tattaaaaaa aaatcttcca aactattttc cagagtgtct gtacctttt 360
E--> 416 acatttccat gagcaacgta tgagtgttt agtttctttg acagcatttg gtatagttac 420
E--> 417 tattttttat ttagttgtt ctcatcctgg acttaatttg aattttccca atgatgagtg 480
418 atgttgaaaa ttttcttgt gcttacttgt catctggata ttctcgtcaa taaaatgtct 540
E--> 419 cttantatcn ttgcccatt ttcaantgga ttctttttgt gttttatcat tgaattttaa 600
E--> 420 gaattcttcn atttatagat atgaattaca gatanaatca tagatattat agatanatat 660
E--> 421 gagttatggg tcacnatt 678
423 <210> SEQ ID NO: 26
424 <211> LENGTH: 509
425 <212> TYPE: PRT
426 <213> ORGANISM: Homo sapiens
428 <400> SEQUENCE: 26

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## RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/032,260

DATE: 02/26/2002

TIME: 11:05:42

Input Set : A:\EP.txt

Output Set: N:\CRF3\02262002\J032260.raw

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429 Met Ala Ala Asp Ser Asp Asp Gly Ala Val Ser Ala Pro Ala Ala Ser
E--> 430      1          5          10          15
431 Asp Gly Gly Val Ser Lys Ser Thr Thr Ser Gly Glu Glu Leu Val Val
E--> 432      20          25          30
433 Gln Val Pro Val Val Asp Val Gln Ser Asn Asn Phe Lys Glu Met Trp
E--> 434      35          40          45
435 Pro Ser Leu Leu Ala Ile Lys Thr Ala Asn Phe Val Ala Val Asp Thr
E--> 436      50          55          60
437 Glu Leu Ser Gly Leu Gly Asp Arg Lys Ser Leu Leu Asn Gln Cys Ile
E--> 438 65          70          75          80
439 Glu Glu Arg Tyr Lys Ala Val Cys His Ala Ala Arg Thr Arg Ser Ile
E--> 440      85          90          95
441 Leu Ser Leu Gly Leu Ala Cys Phe Lys Arg Gln Pro Asp Lys Gly Glu
E--> 442     100         105         110
443 His Ser Tyr Leu Ala Gln Val Phe Asn Leu Thr Leu Leu Cys Met Glu
E--> 444     115         120         125
445 Glu Tyr Val Ile Glu Pro Lys Ser Val Gln Phe Leu Ile Gln His Gly
E--> 446     130         135         140
447 Phe Asn Phe Asn Gln Gln Tyr Ala Gln Gly Ile Pro Tyr His Lys Gly
E--> 448 145         150         155         160
449 Asn Asp Lys Gly Asp Glu Ser Gln Ser Gln Ser Val Arg Thr Leu Phe
E--> 450     165         170         175
451 Leu Glu Leu Ile Arg Ala Arg Arg Pro Leu Val Leu His Asn Gly Leu
E--> 452     180         185         190
453 Ile Asp Leu Val Phe Leu Tyr Gln Asn Phe Tyr Ala His Leu Pro Glu
E--> 454     195         200         205
455 Ser Leu Gly Thr Phe Thr Ala Asp Leu Cys Glu Met Phe Pro Ala Gly
E--> 456     210         215         220
457 Ile Tyr Asp Thr Lys Tyr Ala Ala Glu Phe His Ala Arg Phe Val Ala
E--> 458 225         230         235         240
459 Ser Tyr Leu Glu Tyr Ala Phe Arg Lys Cys Glu Arg Glu Asn Gly Lys
E--> 460     245         250         255
461 Gln Arg Ala Ala Gly Ser Pro His Leu Thr Leu Glu Phe Cys Asn Tyr
E--> 462     260         265         270
463 Pro Ser Ser Met Arg Asp His Ile Asp Tyr Arg Cys Cys Leu Pro Pro
E--> 464     275         280         285
465 Ala Thr His Arg Pro His Pro Thr Ser Ile Cys Asp Asn Phe Ser Ala
E--> 466     290         295         300
467 Tyr Gly Trp Cys Pro Leu Gly Pro Gln Cys Pro Gln Ser His Asp Ile
E--> 468 305         310         315         320
469 Asp Leu Ile Ile Asp Thr Asp Glu Ala Ala Ala Glu Asp Lys Arg Arg
E--> 470     325         330         335
471 Arg Arg Arg Arg Arg Glu Lys Arg Lys Arg Ala Leu Leu Asn Leu Pro
E--> 472     340         345         350
473 Gly Thr Gln Thr Ser Gly Glu Ala Lys Asp Gly Pro Pro Lys Lys Gln
E--> 474     355         360         365
475 Val Cys Gly Asp Ser Ile Lys Pro Glu Glu Thr Glu Gln Glu Val Ala
E--> 476     370         375         380
477 Ala Asp Glu Thr Arg Asn Leu Pro His Ser Lys Gln Gly Asn Lys Asn

```

*misaligned  
amino acid nos.*

*see  
item 3*

*on Enol*

*Summary  
Sheet*

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/032,260

DATE: 02/26/2002

TIME: 11:05:42

Input Set : A:\EP.txt

Output Set: N:\CRF3\02262002\J032260.raw

E--> 478 385 390 395 400  
 479 Asp Leu Glu Met Gly Ile Lys Ala Ala Arg Pro Glu Ile Ala Asp Arg  
 E--> 480 405 410 415  
 481 Ala Thr Ser Glu Val Pro Gly Ser Gln Ala Ser Pro Asn Pro Val Pro  
 E--> 482 420 425 430  
 483 Gly Gly Gly Leu His Arg Ala Gly Phe Asp Ala Phe Met Thr Gly Tyr  
 E--> 484 435 440 445  
 485 Val Met Ala Tyr Val Glu Val Ser Gln Gly Pro Gln Pro Cys Ser Ser  
 E--> 486 450 455 460  
 487 Gly Pro Trp Leu Pro Glu Cys His Asn Lys Val Tyr Leu Ser Gly Lys  
 E--> 488 465 470 475 480  
 489 Ala Val Pro Leu Thr Val Ala Lys Ser Gln Phe Ser Arg Ser Ser Lys  
 E--> 490 485 490 495  
 491 Ala His Asn Gln Lys Met Lys Leu Thr Trp Gly Ser Ser  
 E--> 492 500 505  
 495 <210> SEQ ID NO: 27  
 496 <211> LENGTH: (3938) 3935 (P.7)  
 497 <212> TYPE: DNA  
 498 <213> ORGANISM: Homo sapiens  
 500 <400> SEQUENCE: 27  
 501 agcttatatt ctaatgggga cagaaaagga ataatgaaca taagtaaatt ccataagatg 60  
 502 ttaggtgata aatattagca taaaaagcaa aaattagacc aagaggggaa aaaaaagagt 120  
 503 gccaaagtgg ggtttaatgt tgcaatttta aagactgtgg tcaaggtaga cccaaagcat 180  
 504 tctaagttag tgcaaaggcc ccaaggaggg tgcctggtat gtctgtggta cagtaagtag 240  
 505 gtcaatgtgg ttagaatgga atgagatggg actgagtggg agaagagggtc agagaagtaa 300  
 506 accagatgag gtggggagag gagggtcaca aagtacctta taggccattg gagggatttg 360  
 507 gctgccacac ccttgcctctt agaaggcagt cctcttacta cagccttgca ggtccagtga 420  
 508 tccggggcacc atccgcctca tcccctcact atgctctagc caaggttgac tgaatttagt 480  
 509 tgcttaaaaca cctcaagtgt gtctgcccac cttggggcct cacacaatcc atttcctctg 540  
 510 tttggactct tttatgcttt tacctaacac cttatcattt ttcaagtctt gactgaaatg 600  
 511 tccaaatcag gtcccctcat cttatcctat cacatatttc tgccctgtag ctcttaccta 660  
 512 atgtaatttt acattacttt gattctttcc atcagtgtgt acttcctgaa tttgactgta 720  
 513 aaaaacgact tgagtgcagg gactgattct cttgttgatt ggtgtgtgtc caaagtcagt 780  
 514 gccaggtaaa ctgtacacaa tagatacctg ttaaatgaat taatgggatg ggggatagtc 840  
 515 aaaagagttt ccttttttta ggataggaga aatccaaaga gtttttttat ttttgttttt 900  
 516 tttttgtttg tttgttttgt ttttagagac agtgtgtccc tcactttgct gctctgccac 960  
 517 tcaggctgga gtgcaataag aacatggctc actgcagcct cgacctcctg ggetcaagcc 1020  
 518 atcctctcac ctcagcctcc tgtagctggg actacaggtg cgcaccacca tgcccaacta 1080  
 519 atttttaatt ttctttttgt agagacaagg tttcactatg ttgcccaggc tagtcttgaa 1140  
 520 ctcttagggg caagcgatcc tcccaccttg gcctcctaag atgattacag gccataagcc 1200  
 521 actgcgcccg gcccaagcag ttctgaataa tgatgaaatg ggctcagttg agagaagctg 1260  
 522 aagattaact ataaacaatg agtaacaaag gagcactgga aggcagaggt ggatgggaat 1320  
 523 cgtagtgttt acggaggggac tagtctccaa taggaatttt tttttttttt ttttttttga 1380  
 524 gacggagttt cgtctttgtt gcctaggctg aagtgcacaaa tggcgtgatc tcggctcacc 1440  
 525 gcaacctctg cctcccaggt tcaagcgatt ctccctgcctc agcctcccaa gtagtgggat 1500  
 526 tacaggcgcc cgcaccatac ccagctaatt tttttgtac ttttagtaga gacggggttt 1560  
 527 caccatgttg gccaggtctg ttttgaactc cggacctcag gtaatccgcc cgctcgggcc 1620  
 528 tcccaaagtg ctgggattac aggcgtgagc caccgcgcc ggctaggaa cctctttcaa 1680  
 529 attcaatcac cctctaggtc gactataccg cctagctgct tcacaatttg tcccttctc 1740

same  
error



## RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/032,260

DATE: 02/26/2002

TIME: 11:05:42

Input Set : A:\EP.txt

Output Set: N:\CRF3\02262002\J032260.raw

```

530 gccatccata ctgccagcct taattcaagt tcacattatc acttgattgg attattacaa 1800
531 aagcttccct accaatcggg cgtctttaca ccttgggcag cctcctccga tggcccactc 1860
532 ccgcctcttt tcactttctg gagatcactg agctctccat cctctctggg aattttaccga 1920
533 tgcccagaac gcccttcttt cccccacag accctctcct agtctaactc ctgggcgtgc 1980
E--> 534 ttttaagctca gctcaggca ggcgcacctt ctctggaaag cccaaaccca gccacccca 2040
E--> 535 taccgcgtac ccgcggccca cgtgatgaa gacagcagaa cacggaggcc ccgcgttccc 2100
E--> 536 gccgcgagag caggagagaa agattacctc ccgcgagctc tagcgcgccc ggctttccgg 2160
E--> 537 cgcactccag ggggcgtggc tcgggtccac ccgggctgcg agccggcagc acaggccaat 2220
E--> 538 aggcaattag cgcgcgccag gctgccttcc ccgcgccgga cccgggacgt ctgaacggaa 2280
E--> 539 gttcgacca tccggcgacc gacggcgaga cccgcacca tccccgactg cctgaaccgc 2340
E--> 540 gccaggagac ggaccgcaag tccagcgtac ccacagacga ctcaggcggg agacgagcgg 2400
E--> 541 tgtcatggcc gccgacagtg acgatggcgc agtttcagct cccgcagctt ccgacggtgg 2460
E--> 542 tgtcagcaaa agcacaacat ctgggagga gctagtagtc caggttcccc tagtggatgt 2520
E--> 543 gcaaagcaac aacttcaagg agatgtggc cctcctcct gctagccata aagacagcta 2580
E--> 544 atttcgtggc tgtggacacg gagctgagtg ggcttgggga caggaagagt ttgctgaacc 2640
E--> 545 agtgcatgga ggaacgttac aaggccgtgt gtcatgctgc caggaccgtt tctatccttt 2700
E--> 546 ccctgggcct cgcctgcttc aagcggcagc cagacaaggg tgaacattcc tatctggctc 2760
E--> 547 aagtgttcaa tctcactctg ctgtgcatgg aggagtatgt catagaacca aagtctgtgc 2820
E--> 548 agttcctgat acagcatggc ttcaacttca accagcagta tgcccaaggc atccccctacc 2880
E--> 549 ataagggcaa tgacaagggt gatgagagcc agagccagtc agtacggacc ctattcctgg 2940
E--> 550 agctaattccg agcccgcggg cccctgggtg tacacaatgg ccttatagac ttggtgttcc 3000
E--> 551 tgtaccagaa cttctatgca cacctccctg agagtctggg aaccttcacc gctgacctgt 3060
E--> 552 gtgagatgtt cccagcaggc atttatgaca ccaaatatgc tgetgagttt catgcccgtt 3120
E--> 553 tcgtggcctc ctacttagaa tatgccttcc ggaaatgtga acgggaaaat ggggaagcagc 3180
E--> 554 gggcagctgg cagcccacac cttaccctgg agttctgcaa ctatccttcc agcatgagg 3240
E--> 555 gaccatattg attaccgctg ctgcctgccc ccagcaaccc accgtcctca tcccaccagc 3300
E--> 556 atctgtgaca acttctcggc ttatggctgg tgccccctgg gaccacagtg tctcagctct 3360
E--> 557 cacgatattg accttatcat tgacactgat gaggtgcgg cagaggacaa gcggcgacgg 3420
E--> 558 cgacgacgta gggaaaaacg gaagagggtt ttattgaacct accggggaca cagacctctg 3480
E--> 559 gggaaagctaa ggatggctct cccaagaagc aggtctgtgg ggatagcatc aagcctgaag 3540
E--> 560 aaaccgagca ggaggtggct gccgatgaaa ctaggaacct gcctcactcc aagcaaggca 3600
E--> 561 acaaaaatga cttagagatg gggattaagg cagcaaggcc tgaaatagct gatagagcta 3660
E--> 562 cctcagaagt gccagggagc caagccagtc ctaaccagtc gctgggggtt ggattgcacc 3720
E--> 563 gggctgggtt tgatgccttt atgacaggtt atgtgatggc ctatgtggaa gtgagccagg 3780
E--> 564 gaccgcaacc ctgcagctct ggaccctggc tccctgaatg ccacaataag gtatatttga 3840
E--> 565 gtggcaaagc tgtacccctc acagtggcca agagccagtt ctctcgttcc tccaaagccc 3900
E--> 566 acaatcagaa gatgaagctc acttggggca gtagctga 3938
E--> 569

```

Delete

2039  
↓  
numbering  
off

## VERIFICATION SUMMARY

PATENT APPLICATION: US/10/032,260

DATE: 02/26/2002

TIME: 11:05:43

Input Set : A:\EP.txt

Output Set: N:\CRF3\02262002\J032260.raw

L:12 M:270 C: Current Application Number differs, Replaced Application Number  
 L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
 L:42 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:3 ✓  
 L:54 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:4 ✓  
 M:332 Repeated in SeqNo=4  
 L:66 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:5 ✓  
 L:152 M:283 W: Missing Blank Line separator, <400> field identifier  
 L:171 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:15  
 L:174 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:15  
 L:177 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:15  
 L:180 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:15  
 L:183 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:15  
 L:186 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:15  
 L:189 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:15  
 L:192 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:15  
 L:195 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:15  
 L:198 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:15  
 L:201 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:15  
 L:204 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:15  
 L:207 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:15  
 L:210 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:15  
 L:213 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:15  
 L:228 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:16 ✓  
 M:332 Repeated in SeqNo=16  
 L:264 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:17 ✓  
 M:340 Repeated in SeqNo=17  
 L:274 M:254 E: No. of Bases conflict, LENGTH:Input:660 Counted:659 SEQ:17 ✓  
 M:254 Repeated in SeqNo=17  
 L:276 M:252 E: No. of Seq. differs, <211>LENGTH:Input:725 Found:724 SEQ:17 ✓  
 L:291 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:18 ✓  
 M:340 Repeated in SeqNo=18  
 L:293 M:254 E: No. of Bases conflict, LENGTH:Input:600 Counted:599 SEQ:18 ✓  
 M:254 Repeated in SeqNo=18  
 L:294 M:252 E: No. of Seq. differs, <211>LENGTH:Input:619 Found:618 SEQ:18 ✓  
 L:302 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:19 ✓  
 M:340 Repeated in SeqNo=19  
 L:326 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:20 ✓  
 M:340 Repeated in SeqNo=20  
 L:363 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:22 ✓  
 M:340 Repeated in SeqNo=22  
 L:398 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:24 ✓  
 M:340 Repeated in SeqNo=24  
 L:410 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:25 ✓  
 M:340 Repeated in SeqNo=25  
 L:411 M:254 E: No. of Bases conflict, LENGTH:Input:120 Counted:121 SEQ:25  
 M:254 Repeated in SeqNo=25  
 L:430 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:26  
 M:332 Repeated in SeqNo=26

**VERIFICATION SUMMARY**

PATENT APPLICATION: US/10/032,260

DATE: 02/26/2002

TIME: 11:05:43

Input Set : A:\EP.txt

Output Set: N:\CRF3\02262002\J032260.raw

L:534 M:254 E: No. of Bases conflict, LENGTH:Input:2040 Counted:2039 SEQ:27

M:254 Repeated in SeqNo=27

L:569 M:252 E: No. of Seq. differs, <211>LENGTH:Input:3938 Found:3935 SEQ:27